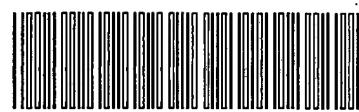


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71 11



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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/966,880A

DATE: 07/19/2002
TIME: 13:48:23

Input Set : A:\06501-088001.txt
Output Set: N:\CRF3\07192002\I966880A.raw

4 <110> APPLICANT: Honjo, Tasuku
5 Muramatsu, Masamichi
7 <120> TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE
10 <130> FILE REFERENCE: 06501-088001
12 <140> CURRENT APPLICATION NUMBER: 09/966,880A
13 <141> CURRENT FILING DATE: 2001-09-28
15 <150> PRIOR APPLICATION NUMBER: PCT/JP00/01918
16 <151> PRIOR FILING DATE: 2000-03-28
18 <150> PRIOR APPLICATION NUMBER: JP 11-371382
19 <151> PRIOR FILING DATE: 1999-12-27
21 <150> PRIOR APPLICATION NUMBER: JP 11-178999
22 <151> PRIOR FILING DATE: 1999-06-24
24 <150> PRIOR APPLICATION NUMBER: JP 11-87192
25 <151> PRIOR FILING DATE: 1999-03-29
27 <160> NUMBER OF SEQ ID NOS: 36
29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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32 <211> LENGTH: 2440
33 <212> TYPE: DNA
34 <213> ORGANISM: Mus musculus
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (93)...(686)
40 <221> NAME/KEY: 5'UTR
41 <222> LOCATION: (1)...(92)
W--> 43 <221> 3'UTR
44 <222> LOCATION: (690)...(2440)
W--> 46 <221> misc_feature
47 <222> LOCATION: (1)...(2440)
48 <223> OTHER INFORMATION: n = A,T,C or G
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52 agggagtcaa gaaagtcacg ctggagaccg at atg gac agc ctt ctg atg aag 113
53 Met Asp Ser Leu Leu Met Lys
54 1 5
56 caa aag aag ttt ctt tac cat ttc aaa aat gtc cgc tgg gcc aag gga 161
57 Gln Lys Lys Phe Leu Tyr His Phe Lys Asn Val Arg Trp Ala Lys Gly
58 10 15 20
60 cgg cat gag acc tac ctc tgc tac gtg gtg aag agg aga gat agt gcc 209
61 Arg His Glu Thr Tyr Leu Cys Tyr Val Val Lys Arg Arg Asp Ser Ala
62 25 30 35
64 acc tcc tgc tca ctg gac ttc ggc cac ctt cgc aac aag tct ggc tgc 257
65 Thr Ser Cys Ser Leu Asp Phe Gly His Leu Arg Asn Lys Ser Gly Cys

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| 66 | 40 | 45 | 50 | 55 | | | | | | | | | | | | | | |
| 68 | cac | gtg | gaa | ttg | ttg | ttc | cta | cgc | tac | atc | tca | gac | tgg | gac | ctg | gac | 305 | |
| 69 | His | Val | Glu | Leu | Leu | Phe | Leu | Arg | Tyr | Ile | Ser | Asp | Trp | Asp | Leu | Asp | | |
| 70 | | | | | | | | | | | | | | | | | | |
| 72 | ccg | ggc | cgg | tgt | tac | cgc | gtc | acc | tgg | ttc | acc | tcc | tgg | agc | ccg | tgc | 353 | |
| 73 | Pro | Gly | Arg | Cys | Tyr | Arg | Val | Thr | Trp | Phe | Thr | Ser | Trp | Ser | Pro | Cys | | |
| 74 | | | | | | | | | | | | | | | | | | |
| 76 | tat | gac | tgt | gcc | cgg | cac | gtg | gct | gag | ttt | ctg | aga | tgg | aac | cct | aac | 401 | |
| 77 | Tyr | Asp | Cys | Ala | Arg | His | Val | Ala | Glu | Phe | Leu | Arg | Trp | Asn | Pro | Asn | | |
| 78 | | | | | | | | | | | | | | | | | | |
| 80 | ctc | agc | ctg | agg | att | ttc | acc | gcg | cgc | ctc | tac | ttc | tgt | gaa | gac | cgc | 449 | |
| 81 | Leu | Ser | Leu | Arg | Ile | Phe | Thr | Ala | Arg | Leu | Tyr | Phe | Cys | Glu | Asp | Arg | | |
| 82 | | | | | | | | | | | | | | | | | | |
| 84 | aag | gct | gag | cct | gag | ggg | ctg | cg | aga | ctg | cac | cgc | gct | ggg | gtc | cag | 497 | |
| 85 | Lys | Ala | Glu | Pro | Glu | Gly | Leu | Arg | Arg | Leu | His | Arg | Ala | Gly | Val | Gln | | |
| 86 | | | | | | | | | | | | | | | | | | |
| 88 | atc | ggg | atc | atg | acc | ttc | aaa | gac | tat | ttt | tac | tgc | tgg | aat | aca | ttt | 545 | |
| 89 | Ile | Gly | Ile | Met | Thr | Phe | Lys | Asp | Tyr | Phe | Tyr | Cys | Trp | Asn | Thr | Phe | | |
| 90 | | | | | | | | | | | | | | | | | | |
| 92 | gta | gaa | aat | cgt | gaa | aga | act | ttc | aaa | gcc | tgg | gaa | ggg | cta | cat | gaa | 593 | |
| 93 | Val | Glu | Asn | Arg | Glu | Arg | Thr | Phe | Lys | Ala | Trp | Glu | Gly | Leu | His | Glu | | |
| 94 | | | | | | | | | | | | | | | | | | |
| 96 | aat | tct | gtc | cg | cta | acc | aga | caa | ctt | cg | cgc | atc | ctt | ttg | ccc | ttg | 641 | |
| 97 | Asn | Ser | Val | Arg | Leu | Thr | Arg | Gln | Leu | Arg | Arg | Ile | Leu | Leu | Pro | Leu | | |
| 98 | | | | | | | | | | | | | | | | | | |
| 100 | tac | gaa | gtc | gat | gac | ttg | cg | gat | gca | ttt | cgt | atg | ttg | gga | ttt | | 686 | |
| 101 | Tyr | Glu | Val | Asp | Asp | Leu | Arg | Asp | Ala | Phe | Arg | Met | Leu | Gly | Phe | | | |
| 102 | | | | | | | | | | | | | | | | | | |
| 104 | tgaaagcaac | ctc | ccttggaaat | gtc | cac | acgtg | atgaaatttc | tct | gaagaga | gtt | ggat | atggat | agaa | ttt | gtt | ggat | 746 | |
| 105 | aaacaaccct | tca | act | atcat | at | gtttttcttc | tta | agtactc | act | tttataa | gtt | ggat | gggg | ttt | gtt | ggat | 806 | |
| 106 | aaatttat | at | ttttttaaa | aaat | actt | gtt | gac | gttgcacagg | acc | ggccagag | caat | gtat | gtta | ttt | gtt | ggat | 866 | |
| 107 | act | gag | ctt | tg | tgca | aca | tc | ggccatct | ct | gggg | aaaca | gcata | actt | tc | cagact | tttgg | 926 | |
| 108 | gtc | gt | gtat | at | gtt | ca | ac | ag | cat | ggaaa | ag | catat | ggaga | ca | cgacc | acaca | 986 | |
| 109 | ttt | gtt | ttt | ca | ac | ag | at | gtt | ca | at | ttt | tct | agg | gtt | atc | agtgtac | 1046 | |
| 110 | gat | tct | ttt | ccct | cta | agg | gtc | ta | ttt | cagg | gg | tc | ttt | ttt | ct | tgt | 1106 | |
| 111 | gggg | gtt | cc | tac | gt | ct | gag | caa | tc | aca | gg | tt | ct | tct | caa | aa | acattaata | 1166 |
| 112 | ctc | agg | gc | cac | ta | gt | ct | gtat | ttt | ttt | ca | ttc | acat | tt | tat | gtt | 1226 | |
| 113 | gg | ctt | gggg | gtt | gg | at | ttt | gca | tc | gg | ct | ttt | ttt | ttt | ttt | ttt | 1286 | |
| 114 | taaaat | gt | cac | at | gagg | act | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | 1346 | |
| 115 | caa | at | ccc | cc | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | 1406 | |
| 116 | ttat | ca | aa | ga | ag | at | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | 1466 | |
| 117 | at | taa | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | 1526 | |
| 118 | gaga | aa | agg | gg | ca | aa | gg | at | cc | aa | gg | tt | tt | tt | tt | tt | 1586 | |
| 119 | tc | gtt | ttt | cc | ttt | cc | aa | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | 1646 | |
| 120 | acc | ac | gg | gg | tt | at | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | 1706 | |
| 121 | cgc | ca | gag | ag | at | g | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | 1766 | |
| 122 | ttt | gg | aa | ca | ttt | aa | gg | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | 1826 | |
| 123 | gtc | ttt | gg | tt | at | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | 1886 | |
| 124 | aat | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | ttt | 1946 | |

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|----------|-------------|---|-------------|------------|--------------|-----------------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 125 | gtggcaaaat | agggaaaagt | gcattcacct | atagttccag | cattcaggaa | gctgaggcag | 2006 | | | | | | | | | |
| 126 | gaggattgt | aatttgaggc | cagtctgagc | tgtaaggtga | gaccctat | ttt caaacaacac | 2066 | | | | | | | | | |
| 127 | agccagaatt | gggttctgg | taatcatact | taacaaggga | aaaatgc | aaag acgcaagacc | 2126 | | | | | | | | | |
| 128 | gtggcaagg | aatgacgctt | tgcccaacga | aatgtaggaa | accaacat | actccagtt | 2186 | | | | | | | | | |
| 129 | tgtccctctt | tatgtctgg | ctccctaaca | acgatctt | g ctaatgagaa | aaatattaga | 2246 | | | | | | | | | |
| 130 | aaaaaaat | cctgtcaat | tatcacccag | tcgcattat | aatgcattt | aaaggcccac | 2306 | | | | | | | | | |
| 131 | aagaaaat | ctcgtcaat | tatcacccag | tcgcattat | aatgcattt | aaaggcccac | 2366 | | | | | | | | | |
| W--> 132 | aaaaataaaag | atcatccatt | cttcctgca | aaaaaaaaaa | aaaaaanaaa | aaaaaaaaaa | 2426 | | | | | | | | | |
| 133 | aaaaaaaaaa | aaaa | | | | | 2440 | | | | | | | | | |
| 135 | <210> | SEQ ID NO: 2 | | | | | | | | | | | | | | |
| 136 | <211> | LENGTH: 198 | | | | | | | | | | | | | | |
| 137 | <212> | TYPE: PRT | | | | | | | | | | | | | | |
| 138 | <213> | ORGANISM: Mus musculus | | | | | | | | | | | | | | |
| 140 | <400> | SEQUENCE: 2 | | | | | | | | | | | | | | |
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| 142 | 1 | | | | | 5 | | | | 10 | | | | 15 | | |
| 143 | Asn | Val | Arg | Trp | Ala | Lys | Gly | Arg | His | Glu | Thr | Tyr | Leu | Cys | Tyr | Val |
| 144 | | | | | | 20 | | | | 25 | | | | 30 | | |
| 145 | Val | Lys | Arg | Arg | Asp | Ser | Ala | Thr | Ser | Cys | Ser | Leu | Asp | Phe | Gly | His |
| 146 | | | | | | 35 | | | | 40 | | | | 45 | | |
| 147 | Leu | Arg | Asn | Lys | Ser | Gly | Cys | His | Val | Glu | Leu | Leu | Phe | Leu | Arg | Tyr |
| 148 | | | | | | 50 | | | | 55 | | | | 60 | | |
| 149 | Ile | Ser | Asp | Trp | Asp | Leu | Asp | Pro | Gly | Arg | Cys | Tyr | Arg | Val | Thr | Trp |
| 150 | 65 | | | | | 65 | | | | 70 | | | | 75 | | 80 |
| 151 | Phe | Thr | Ser | Trp | Ser | Pro | Cys | Tyr | Asp | Cys | Ala | Arg | His | Val | Ala | Glu |
| 152 | | | | | | 85 | | | | 90 | | | | 95 | | |
| 153 | Phe | Leu | Arg | Trp | Asn | Pro | Asn | Leu | Ser | Leu | Arg | Ile | Phe | Thr | Ala | Arg |
| 154 | | | | | | 100 | | | | 105 | | | | 110 | | |
| 155 | Leu | Tyr | Phe | Cys | Glu | Asp | Arg | Lys | Ala | Glu | Pro | Glu | Gly | Leu | Arg | Arg |
| 156 | | | | | | 115 | | | | 120 | | | | 125 | | |
| 157 | Leu | His | Arg | Ala | Gly | Val | Gln | Ile | Gly | Ile | Met | Thr | Phe | Lys | Asp | Tyr |
| 158 | | | | | | 130 | | | | 135 | | | | 140 | | |
| 159 | Phe | Tyr | Cys | Trp | Asn | Thr | Phe | Val | Glu | Asn | Arg | Glu | Arg | Thr | Phe | Lys |
| 160 | 145 | | | | | 145 | | | | 150 | | | | 155 | | 160 |
| 161 | Ala | Trp | Glu | Gly | Leu | His | Glu | Asn | Ser | Val | Arg | Leu | Thr | Arg | Gln | Leu |
| 162 | | | | | | 165 | | | | 170 | | | | 175 | | |
| 163 | Arg | Arg | Ile | Leu | Leu | Pro | Leu | Tyr | Glu | Val | Asp | Asp | Leu | Arg | Asp | Ala |
| 164 | | | | | | 180 | | | | 185 | | | | 190 | | |
| 165 | Phe | Arg | Met | Leu | Gly | Phe | | | | | | | | | | |
| 166 | | | | | 195 | | | | | | | | | | | |
| 168 | <210> | SEQ ID NO: 3 | | | | | | | | | | | | | | |
| 169 | <211> | LENGTH: 30 | | | | | | | | | | | | | | |
| 170 | <212> | TYPE: DNA | | | | | | | | | | | | | | |
| 171 | <213> | ORGANISM: Artificial Sequence | | | | | | | | | | | | | | |
| 173 | <220> | FEATURE: | | | | | | | | | | | | | | |
| 174 | <223> | OTHER INFORMATION: Artificially synthesized primer sequence, AID138 | | | | | | | | | | | | | | |
| 178 | <400> | SEQUENCE: 3 | | | | | | | | | | | | | | |
| 179 | ggaattcgcc | atggacagcc | ttctgtatgaa | | | | | | | | | | | | | 30 |
| 181 | <210> | SEQ ID NO: 4 | | | | | | | | | | | | | | |

RAW SEQUENCE LISTING
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183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Artificially synthesized primer sequence, AID161
191 <400> SEQUENCE: 4
192 gcccgtcgag tcaaaatccc aacatacgaa 30
194 <210> SEQ ID NO: 5
195 <211> LENGTH: 25
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Artificially synthesized primer sequence, AID118
204 <400> SEQUENCE: 5
205 ggctgaggtt agggttccat ctcag 25
207 <210> SEQ ID NO: 6
208 <211> LENGTH: 25
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Artificially synthesized primer sequence, AID119
217 <400> SEQUENCE: 6
218 gagggagtca agaaagtac gctgg 25
220 <210> SEQ ID NO: 7
221 <211> LENGTH: 2818
222 <212> TYPE: DNA
223 <213> ORGANISM: Homo sapiens
225 <220> FEATURE:
226 <221> NAME/KEY: CDS
227 <222> LOCATION: (80)...(673)
229 <221> NAME/KEY: 5'UTR
230 <222> LOCATION: (1)...(79)
W--> 232 <221> 3'UTR
233 <222> LOCATION: (677)...(2818)
W--> 235 <400> 7
236 agagaaccat cattaattga agtgagattt ttctggcctg agacttgcag ggaggcaaga 60
237 agacactctg gacaccact atg gac agc ctc ttg atg aac cgg agg aag ttt 112
238 Met Asp Ser Leu Leu Met Asn Arg Arg Lys Phe
239 1 5 10
241 ctt tac caa ttc aaa aat gtc cgc tgg gct aag ggt cgg cgt gag acc 160
242 Leu Tyr Gln Phe Lys Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr
243 15 20 25
245 tac ctg tgc tac gta gtg aag agg cgt gac agt gct aca tcc ttt tca 208
246 Tyr Leu Cys Tyr Val Val Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser
247 30 35 40
249 ctg gac ttt ggt tat ctt cgc aat aag aac ggc tgc cac gtg gaa ttg 256
250 Leu Asp Phe Gly Tyr Leu Arg Asn Lys Asn Gly Cys His Val Glu Leu
251 45 50 55
253 ctc ttc ctc cgc tac atc tcg gac tgg gac cta gac cct ggc cgc tgc 304

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|-----|-------------|-------------|-------------|------------|------------|-------------|-----|-----|-----|-----|-----|------------|------------|-----|-----|-----|------|
| 254 | Leu | Phe | Leu | Arg | Tyr | Ile | Ser | Asp | Trp | Asp | Leu | Asp | Pro | Gly | Arg | Cys | |
| 255 | 60 | | | | | | 65 | | | | 70 | | | | 75 | | |
| 257 | tac | cgc | gtc | acc | tgg | ttc | acc | tcc | tgg | agc | ccc | tgc | tac | gac | tgt | gcc | 352 |
| 258 | Tyr | Arg | Val | Thr | Trp | Phe | Thr | Ser | Trp | Ser | Pro | Cys | Tyr | Asp | Cys | Ala | |
| 259 | | | | | | | | | | | 80 | | | 85 | | 90 | |
| 261 | cga | cat | gtg | gcc | gac | ttt | ctg | cga | ggg | aac | ccc | aac | ctc | agt | ctg | agg | 400 |
| 262 | Arg | His | Val | Ala | Asp | Phe | Leu | Arg | Gly | Asn | Pro | Asn | Leu | Ser | Leu | Arg | |
| 263 | | | | | | | | | | | 95 | | | 100 | | 105 | |
| 265 | atc | ttc | acc | gcg | cgc | ctc | tac | ttc | tgt | gag | gac | cgc | aag | gct | gag | ccc | 448 |
| 266 | Ile | Phe | Thr | Ala | Arg | Leu | Tyr | Phe | Cys | Glu | Asp | Arg | Lys | Ala | Glu | Pro | |
| 267 | | | | | | | | | | | 110 | | | 115 | | 120 | |
| 269 | gag | ggg | ctg | cgg | cg | ctg | cac | cgc | gcc | ggg | gtg | caa | ata | gcc | atc | atg | 496 |
| 270 | Glu | Gly | Leu | Arg | Arg | Leu | His | Arg | Ala | Gly | Val | Gln | Ile | Ala | Ile | Met | |
| 271 | | | | | | | | | | | 125 | | | 130 | | 135 | |
| 273 | acc | ttc | aaa | gat | tat | ttt | tac | tgc | tgg | aat | act | ttt | gta | gaa | aac | cat | 544 |
| 274 | Thr | Phe | Lys | Asp | Tyr | Phe | Tyr | Cys | Trp | Asn | Thr | Phe | Val | Glu | Asn | His | |
| 275 | | | | | | | | | | | 140 | | | 145 | | 150 | 155 |
| 277 | gaa | aga | act | ttc | aaa | gcc | tgg | gaa | ggg | ctg | cat | gaa | aat | tca | gtt | cgt | 592 |
| 278 | Glu | Arg | Thr | Phe | Lys | Ala | Trp | Glu | Gly | Leu | His | Glu | Asn | Ser | Val | Arg | |
| 279 | | | | | | | | | | | 160 | | | 165 | | 170 | |
| 281 | ctc | tcc | aga | cag | ctt | cg | cgc | atc | ctt | ttg | ccc | ctg | tat | gag | gtt | gat | 640 |
| 282 | Leu | Ser | Arg | Gln | Leu | Arg | Arg | Ile | Leu | Leu | Pro | Leu | Tyr | Glu | Val | Asp | |
| 283 | | | | | | | | | | | 175 | | | 180 | | 185 | |
| 285 | gac | tta | cga | gac | gca | ttt | cgt | act | ttg | gga | ctt | tgatagcaac | ttccaggaat | | | | 693 |
| 286 | Asp | Leu | Arg | Asp | Ala | Phe | Arg | Thr | Leu | Gly | Leu | | | | | | |
| 287 | | | | | | | | | | | 190 | | | 195 | | | |
| 289 | gtcacacacg | atgaaatatac | tctgctgaag | acagtggata | aaaaacagtc | cttcaagtct | | | | | | | | | | | 753 |
| 290 | tctctgtttt | tattcttcaa | ctctcacttt | cttagagttt | acagaaaaaa | tatttatata | | | | | | | | | | | 813 |
| 291 | cgactctta | aaaagatcta | tgtcttggaa | atagagaagg | aacacaggtc | tggccagggaa | | | | | | | | | | | 873 |
| 292 | cgtgctgcaa | ttgggtgcagt | tttgaatgca | acatgtccc | ctactggaa | taacagaact | | | | | | | | | | | 933 |
| 293 | gcaggacctg | ggagcatcct | aaagtgtcaa | cgttttctaa | tgacttttag | gtaggatgag | | | | | | | | | | | 993 |
| 294 | agcagaaggt | agatcctaaa | aagcatggtg | agaggatcaa | atgtttttat | atcaacatcc | | | | | | | | | | | 1053 |
| 295 | tttattattt | gattcatttg | agttAACAGT | ggtgttagtg | atagattttt | ctattctttt | | | | | | | | | | | 1113 |
| 296 | cccttgacgt | ttacttcaa | gtAACACAAA | ctctccatc | aggccatgat | ctataggacc | | | | | | | | | | | 1173 |
| 297 | tcctaatttgg | agtatctggg | tgattgtgac | cccaaaccat | ctctccaaag | cattaatatac | | | | | | | | | | | 1233 |
| 298 | caatcatgcg | ctgtatgttt | taatcagcag | aagcatgttt | ttatgtttgt | acaaaagaag | | | | | | | | | | | 1293 |
| 299 | attgttatgg | gtggggatgg | aggtatagac | catgcattgt | caccccaag | ctactttat | | | | | | | | | | | 1353 |
| 300 | aaaggatctt | aaaatgggca | ggaggactgt | gaacaagaca | ccctaataat | gggtttagt | | | | | | | | | | | 1413 |
| 301 | ctgaagtagc | aaatcttctg | gaaacgcaa | ctcttttaag | gaagtccta | atttagaaac | | | | | | | | | | | 1473 |
| 302 | acccacaaac | ttcacatatac | ataatttgc | aacaatttgg | aggaagtgc | ttgaatgttg | | | | | | | | | | | 1533 |
| 303 | gggagaggaa | aatctatttg | ctctcggtgg | tcttttcatc | tcagaaatgc | caatcaggc | | | | | | | | | | | 1593 |
| 304 | aaggtttgc | acattttgc | tgtgtgtat | gtttttccca | aaggatattt | aactatataa | | | | | | | | | | | 1653 |
| 305 | gagagttgt | acaaaacaga | atgataaaagc | tgcgaaccgt | ggcacacgt | catagttcta | | | | | | | | | | | 1713 |
| 306 | gctgcttggg | aggttgagga | gggaggatgg | tttgcacaca | ggtgtcaag | gccaggctgg | | | | | | | | | | | 1773 |
| 307 | gcaacataac | aagatccgt | ctctcaaaaa | aaaaaaa | aaaaagaaag | agagaggggcc | | | | | | | | | | | 1833 |
| 308 | gggcgtgg | gctcacgcct | gtatcccaag | cacttggg | ggccgagccg | ggccgatcac | | | | | | | | | | | 1893 |
| 309 | ctgtggtcag | gagtttgaga | ccagcctggc | caacatggca | aaacccgtc | tgtactcaaa | | | | | | | | | | | 1953 |
| 310 | atgcaaaaat | tagccaggcg | ttgttagcagg | cacctgtat | cccagctact | tggaggcgt | | | | | | | | | | | 2013 |
| 311 | aggcaggaga | atcgottgaa | cccaggaggt | ggaggttgca | gttagctgag | atcggtccgt | | | | | | | | | | | 2073 |

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/19/2002
PATENT APPLICATION: US/09/966,880A TIME: 13:48:24

Input Set : A:\06501-088001.txt
Output Set: N:\CRF3\07192002\I966880A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2413

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/966,880A

DATE: 07/19/2002
TIME: 13:48:24

Input Set : A:\06501-088001.txt
Output Set: N:\CRF3\07192002\I966880A.raw

L:43 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:46 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:50 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2366
L:232 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:235 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:371 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:374 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9